

# SEQUENCE LISTING

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<1> IDENTIFICATION OF A LARGE NUMBER OF BIOLOGICAL (MICRO)ORGANISMS GROUPS AT DIFFERENT LEVELS BY THEIR DETECTION ON A SAME ARRAY

4-10 JANM213.CC1CP1

4100 EP 00870055.1  
2010-03-24

REF 00870-04.5  
0010-03-34

151 - PS 09/817,014  
151 - 1081-03-23

2000 321

FastSEQ for Windows Version 4.0

1

Figure 1: Schematic representation of the experimental design. The diagram shows a sequence of events: 'Stimulus' (a box with a question mark), 'Response' (a box with a question mark), 'Feedback' (a box with a question mark), and 'Outcome' (a box with a question mark). Arrows indicate the flow from Stimulus to Response, Response to Feedback, and Feedback to Outcome. A feedback loop arrow connects Outcome back to Stimulus. The entire process is labeled 'Trial'.

017-01A

Artificial Sequence

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403.3

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100

. . . CNA

Artificial Sequence

100

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42

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211, 23

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1113  
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23

1114  
1115  
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1118 primer for amplification of *S. epidermidis*

1119  
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22

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1125  
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24

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25

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capture probe Mage 6 DTS06

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capture probe Mage 7 DTAS07

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Seq 116  
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Seq 117  
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Seq 118  
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415 capture probe HTR2C/1C

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acactttgct tt

22

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421 DNA  
422 Artificial Sequence

423  
424 capture probe HTR1B

425 151

20

426 gataaacac cgcacagtg

427

428 429 152

430 431 19

432 433 DNA

434 435 Artificial Sequence

436

437 438

439 440 capture probe HTR1D

441

442 443 152

19

444 gataacagg gcacgggtg

445

446 447 153

448 449 20

450 451 DNA

452 453 Artificial Sequence

454

455 456

457 458 capture probe HTR1A

459 153

20

460 gataacat aggtcgggtg

461 154

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469 154

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449 capture probe HLA-A68 ITSA68A

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- 1113 27
- 1114 DNA
- 1115 Artificial Sequence

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101 1111 15
102 1112 DNA
103 1113 Artificial Sequence

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... sense primer for cytochrome P450

1400- 133  
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120
121 primer consensus a3, a23, a1, a2 antisense

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134  
ttaacagaga

- 185
- 19
- DNA
- Artificial Sequence

primer Specific a9 antisense

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21

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4400-198  
4400-199  
4400-200 Artificial Sequence

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4400 consensus primer OPTE92 (T-E9) Reverse

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21

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4400-200  
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4400 consensus primer OPLB1 (octopine Left Border)  
Forward

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25

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4400-201  
4400-202 Artificial Sequence

4400  
4400 consensus primer OPEPS4 (EPSPS) Reverse

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ggtatggttg gcatcttggt

20

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| <400> 113                            | 28 |
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4111-156  
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4111-157  
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4111-160  
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24

4111-163  
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24

4111-168  
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24

4111-173  
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4111-176  
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24

4111-178

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4121-  
 4122-Fish2 consensus primer

4123-20  
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4130-270  
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4131-271  
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4137-271  
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4138-272  
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4144-272  
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aaagcraat cagtcggcct taattgca

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\*407-286  
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\*409-DNA  
\*410-Artificial Sequence

\*411-287  
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\*413-285  
aaagctatt cagttggcct caactgta

28

\*414-286  
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\*416-DNA  
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\*418-287  
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\*420-286  
aaagcctact cagtaggcct caaatgca

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\*421-287  
\*422-40  
\*423-DNA  
\*424-Artificial Sequence

\*425-288  
\*426-Salmonidae family capture nucleotide sequence

\*427-287  
aaagctaac gctaacggag catctttcct ctttatctgt

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\*428-288  
\*429-40  
\*430-DNA  
\*431-Artificial Sequence

\*432-289  
\*433-Pleuronectidae family capture nucleotide sequence

\*434-288

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<213> antisense consensus primer, S. saprophyticus

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gtatgagga artagaa

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<110> 316

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4114  
4115 S. agalactiae capture probe

4116 21  
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4117 317  
4118 20  
4119 DNA  
4120 Artificial Sequence

4121  
4122 S. aureus capture probe

4400 317  
gggttatatg acacatctaa

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4123 318  
4124 20  
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4126 Artificial Sequence

4127  
4128 S. epidermidis capture probe

4400 318  
gtaatgaacga aacttctaaa

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4129 319  
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4132 Artificial Sequence

4133  
4134 S. haemolyticus capture probe

4400 319  
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